RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/594,417_

Source: _TFWO_

Date Processed by STIC: _10/26/06_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/594, 417_   CRF Edit Date: _10/26/06_
Edited by: _____.

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_✓_ Deleted: _✓_ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 10/26/2006
PATENT APPLICATION: US/10/594,417   TIME: 11:46:12

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\10262006\J594417.raw

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 3 <110> APPLICANT: NIPPON SHOKUBAI CO., LTD.
 5 <120> TITLE OF INVENTION: Method for producing 1,3-propanediol and 3-hydroxypropionic
acid
 7 <130> FILE REFERENCE: PH-2376-PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/594,417
C--> 9 <141> CURRENT FILING DATE: 2006-09-26
 9 <150> PRIOR APPLICATION NUMBER: JP 2004-093417
10 <151> PRIOR FILING DATE: 2004-03-26
12 <150> PRIOR APPLICATION NUMBER: JP 2004-124524
13 <151> PRIOR FILING DATE: 2004-04-20
15 <160> NUMBER OF SEQ ID NOS: 75
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 558
21 <212> TYPE: PRT
22 <213> ORGANISM: Lactobacillus reuteri
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30 Gln Asp Thr Phe Val Lys Glu Trp Pro Glu Glu Gly Phe Val Ala Met
31              20                  25                  30
34 Met Gly Pro Asn Asp Pro Lys Pro Ser Val Lys Val Glu Asn Gly Lys
35          35                  40                  45
38 Ile Val Glu Met Asp Gly Lys Lys Leu Glu Asp Phe Asp Leu Ile Asp
39      50                  55                  60
42 Leu Tyr Ile Ala Lys Tyr Gly Ile Asn Ile Asp Asn Val Glu Lys Val
43 65                  70                  75                  80
46 Met Asn Met Asp Ser Thr Lys Ile Ala Arg Met Leu Val Asp Pro Asn
47              85                  90                  95
50 Val Ser Arg Asp Glu Ile Ile Glu Ile Thr Ser Ala Leu Thr Pro Ala
51              100                 105                 110
54 Lys Ala Glu Glu Ile Ile Ser Lys Leu Asp Phe Gly Glu Met Ile Met
55          115                 120                 125
58 Ala Val Lys Lys Met Arg Pro Arg Arg Lys Pro Asp Asn Gln Cys His
59      130                 135                 140
62 Val Thr Asn Thr Val Asp Asn Pro Val Gln Ile Ala Ala Asp Ala Ala
63 145                 150                 155                 160
66 Asp Ala Ala Leu Arg Gly Phe Pro Glu Gln Glu Thr Thr Thr Ala Val
67              165                 170                 175
70 Ala Arg Tyr Ala Pro Phe Asn Ala Ile Ser Ile Leu Ile Gly Ala Gln
71          180                 185                 190
74 Thr Gly Arg Pro Gly Val Leu Thr Gln Cys Ser Val Glu Glu Ala Thr
75          195                 200                 205
78 Glu Leu Gln Leu Gly Met Arg Gly Phe Thr Ala Tyr Ala Glu Thr Ile
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 79      210                    215                    220
 82 Ser Val Tyr Gly Thr Asp Arg Val Phe Thr Asp Gly Asp Asp Thr Pro
 83 225                    230                    235                    240
 86 Trp Ser Lys Gly Phe Leu Ala Ser Cys Tyr Ala Ser Arg Gly Leu Lys
 87                 245                    250                    255
 90 Met Arg Phe Thr Ser Gly Ala Gly Ser Glu Val Leu Met Gly Tyr Pro
 91                 260                    265                    270
 94 Glu Gly Lys Ser Met Leu Tyr Leu Glu Ala Arg Cys Ile Leu Leu Thr
 95            275                    280                    285
 98 Lys Ala Ser Gly Val Gln Gly Leu Gln Asn Gly Ala Val Ser Cys Ile
 99      290                    295                    300
102 Glu Ile Pro Gly Ala Val Pro Asn Gly Ile Arg Glu Val Leu Gly Glu
103 305                    310                    315                    320
106 Asn Leu Leu Cys Met Met Cys Asp Ile Glu Cys Ala Ser Gly Cys Asp
107                 325                    330                    335
110 Gln Ala Tyr Ser His Ser Asp Met Arg Arg Thr Glu Arg Phe Ile Gly
111                 340                    345                    350
114 Gln Phe Ile Ala Gly Thr Asp Tyr Ile Asn Ser Gly Tyr Ser Ser Thr
115            355                    360                    365
118 Pro Asn Tyr Asp Asn Thr Phe Ala Gly Ser Asn Thr Asp Ala Met Asp
119      370                    375                    380
122 Tyr Asp Asp Met Tyr Val Met Glu Arg Asp Leu Gly Gln Tyr Tyr Gly
123 385                    390                    395                    400
126 Ile His Pro Val Lys Glu Glu Thr Ile Ile Lys Ala Arg Asn Lys Ala
127                 405                    410                    415
130 Ala Lys Ala Leu Gln Ala Val Phe Glu Asp Leu Gly Leu Pro Lys Ile
131                 420                    425                    430
134 Thr Asp Glu Glu Val Glu Ala Ala Thr Tyr Ala Asn Thr His Asp Asp
135            435                    440                    445
138 Met Pro Lys Arg Asp Met Val Ala Asp Met Lys Ala Ala Gln Asp Met
139      450                    455                    460
142 Met Asp Arg Gly Ile Thr Ala Ile Asp Ile Ile Lys Ala Leu Tyr Asn
143 465                    470                    475                    480
146 His Gly Phe Lys Asp Val Ala Glu Ala Ile Leu Asn Leu Gln Lys Gln
147                 485                    490                    495
150 Lys Val Val Gly Asp Tyr Leu Gln Thr Ser Ser Ile Phe Asp Lys Asp
151            500                    505                    510
154 Trp Asn Val Thr Ser Ala Val Asn Asp Gly Asn Asp Tyr Gln Gly Pro
155      515                    520                    525
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162 Lys Asp Leu Pro Phe Ala Leu Asp Pro Glu His Leu Glu Leu
163 545                    550                    555
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 1677
168 <212> TYPE: DNA
169 <213> ORGANISM: Lactobacillus reuteri
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176 agtgtaaaag ttgaaaatgg caagatcgta gagatggatg gtaaaaagct cgaagatttt  180
178 gatttgattg acttgtacat tgctaagtat ggaatcaata ttgacaacgt tgaaaaagtt  240
180 atgaatatgg attctaccaa gattgcacgg atgcttgttg atcctaatgt ttctcgtgat  300
182 gaaattattg aaattacatc agctttgact cctgctaagg ctgaagagat catcagtaag  360
184 cttgattttg gtgaaatgat tatggctgtc aagaagatgc gcccacgtcg taagcctgac  420
186 aaccagtgtc acgttaccaa tactgttgat aacccagttc aaattgctgc tgatgctgct  480
188 gatgccgctc ttcgtggatt tccagaacaa gaaaccacga cagctgtggc acgttatgca  540
190 ccattcaatg ctatttcaat tttaattggt gcacaaacag gtcgccctgg tgtattgaca  600
192 caatgttctg ttgaagaagc tactgaattg caattaggta tgcgtggttt taccgcatat  660
194 gctgaaacca tttcagttta cggtactgat cgtgtattta ccgatggtga tgatactcca  720
196 tggtctaaag gcttcttggc atcttgttat gcatcacgtg gtttgaagat gcgatttact  780
198 tcaggtgccg gttcagaagt tttgatgggt tatccagaag gtaagtcaat gctttacctt  840
200 gaagcgcgtt gtattttact tactaaggct tcaggtgttc aaggacttca aaatggtgcc  900
202 gtaagttgta ttgaaattcc tggtgctgtt cctaatggta ttcgtgaagt tctcggtgaa  960
204 aacttgttat gtatgatgtg tgacatcgaa tgtgcttctg gttgtgacca agcatactca  1020
206 cactccgata tgcggcggac tgaacggttt attggtcaat ttattgccgg tactgattat  1080
208 attaactctg gttactcatc aactcctaac tacgataata ccttcgctgg ttcaaacact  1140
210 gatgctatgg actacgatga tatgtatgtt atggaacgtg acttgggtca atattatggt  1200
212 attcaccctg ttaaggaaga aaccattatt aaggcacgta taaggccgc taaagccctt  1260
214 caagcagtat ttgaagatct tggattacca aagattactg atgaagaggt cgaagcagca  1320
216 acgtatgcta cacccatga tgacatgcca aagcgggata tggttgcaga tatgaaggct  1380
218 gctcaagata tgatggatcg tggaattact gctattgata ttatcaaggc attgtacaac  1440
220 cacggattta agatgtcgc tgaagcaatt ttgaaccttc aaaaacaaaa agttgttggt  1500
222 gattaccttc aaacatcttc tattttgat aaagattgga cgtcacttc tgctgttaac  1560
224 gacggaaatg attatcaagg accaggtact ggataccgtc tatatgaaga caaggaagaa  1620
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230 <211> LENGTH: 558
231 <212> TYPE: PRT
232 <213> ORGANISM: Lactobacillus reuteri
234 <400> SEQUENCE: 3
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237 1               5                  10                  15
240 Gln Asp Thr Phe Val Lys Glu Trp Pro Glu Glu Gly Phe Val Ala Met
241             20                  25                  30
244 Met Gly Pro Asn Asp Pro Lys Pro Ser Val Lys Val Glu Asn Gly Lys
245             35                  40                  45
248 Ile Val Glu Met Asp Gly Lys Lys Arg Glu Asp Phe Asp Leu Ile Asp
249     50                  55                  60
252 Leu Tyr Ile Ala Lys Tyr Gly Ile Asn Ile Asp Asn Val Glu Lys Val
253 65                  70                  75                  80
256 Met Asn Met Asp Ser Thr Lys Ile Ala Arg Met Leu Val Asp Pro Asn
257             85                  90                  95
260 Val Ser Arg Glu Ser Ile Ile Glu Ile Thr Ser Ala Leu Thr Pro Ala
261             100                 105                 110
264 Lys Ala Glu Glu Ile Ile Ser Lys Leu Asp Phe Gly Glu Met Ile Met
265         115                 120                 125
268 Ala Ile Lys Lys Met Arg Pro Arg Arg Lys Pro Asp Asn Gln Cys His
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269      130                    135                    140
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277                    165                    170                    175
280 Ala Arg Tyr Ala Pro Phe Asn Ala Ile Ser Ile Leu Ile Gly Ala Gln
281                    180                    185                    190
284 Thr Gly Arg Pro Gly Val Leu Thr Gln Cys Ser Val Glu Glu Ala Thr
285                    195                    200                    205
288 Glu Leu Gln Leu Gly Met Arg Gly Phe Thr Ala Tyr Ala Glu Thr Ile
289      210                    215                    220
292 Ser Val Tyr Gly Thr Asp Arg Val Phe Thr Asp Gly Asp Asp Thr Pro
293 225                    230                    235                    240
296 Trp Ser Lys Gly Phe Leu Ala Ser Cys Tyr Ala Ser Arg Gly Leu Lys
297                    245                    250                    255
300 Met Arg Phe Thr Ser Gly Ala Gly Ser Glu Val Leu Met Gly Tyr Pro
301                    260                    265                    270
304 Glu Gly Lys Ser Met Leu Tyr Leu Glu Ala Arg Cys Ile Leu Leu Thr
305      275                    280                    285
308 Lys Ala Ser Gly Val Gln Gly Leu Gln Asn Gly Ala Val Ser Cys Ile
309      290                    295                    300
312 Glu Ile Pro Gly Ala Val Pro Asn Gly Ile Arg Glu Val Leu Gly Glu
313 305                    310                    315                    320
316 Asn Leu Leu Cys Met Met Cys Asp Ile Glu Cys Ala Ser Gly Cys Asp
317                    325                    330                    335
320 Gln Ala Tyr Ser His Ser Asp Met Arg Arg Thr Glu Arg Phe Ile Gly
321                    340                    345                    350
324 Gln Phe Ile Ala Gly Thr Asp Tyr Ile Asn Ser Gly Tyr Ser Ser Thr
325                    355                    360                    365
328 Pro Asn Tyr Asp Asn Thr Phe Ala Gly Ser Asn Thr Asp Ala Met Asp
329      370                    375                    380
332 Tyr Asp Asp Met Tyr Val Met Glu Arg Asp Leu Gly Gln Tyr Tyr Gly
333 385                    390                    395                    400
336 Ile His Pro Val Gln Glu Glu Thr Ile Ile Lys Ala Arg Asn Lys Ala
337                    405                    410                    415
340 Ala Lys Ala Leu Gln Ala Val Phe Glu Asp Leu Gly Leu Pro Lys Ile
341                    420                    425                    430
344 Thr Asp Glu Glu Val Glu Ala Ala Thr Tyr Ala Asn Thr His Asp Asp
345      435                    440                    445
348 Met Pro Lys Arg Asp Met Val Ala Asp Met Lys Ala Ala Gln Asp Met
349      450                    455                    460
352 Met Asp Arg Gly Ile Thr Ala Ile Asp Ile Ile Lys Ala Leu Tyr Asn
353 465                    470                    475                    480
356 His Gly Phe Lys Asp Val Ala Glu Ala Val Leu Asn Leu Gln Lys Gln
357                    485                    490                    495
360 Lys Val Val Gly Asp Tyr Leu Gln Thr Ser Ser Ile Phe Asp Lys Asp
361                    500                    505                    510
364 Trp Asn Ile Thr Ser Ala Val Asn Asp Gly Asn Asp Tyr Gln Gly Pro
365                    515                    520                    525
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368 Gly Thr Gly Tyr Arg Leu Tyr Glu Asp Lys Glu Glu Trp Asp Arg Ile
369     530                 535                 540
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373 545                 550                 555
376 <210> SEQ ID NO: 4
377 <211> LENGTH: 1677
378 <212> TYPE: DNA
379 <213> ORGANISM: Lactobacillus reuteri
381 <400> SEQUENCE: 4
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386 agtgtaaagg ttgaaaacgg taaaattgtc gaaatggatg gcaagaagcg ggaagacttt   180
388 gacttaattg acctctacat tgctaagtat ggaattaata ttgataacgt tgaaaaagtt   240
390 atgaatatgg attcaactaa aattgcacgg atgttggttg atccaaatgt ctcacgtgaa   300
392 tccatcattg aaattacttc tgcactaact ccagcgaaag ccgaagaaat cattagtaag   360
394 cttgactttg gtgaaatgat tatggctatc aagaagatgc gtccgcgtcg gaagccggat   420
396 aaccaatgtc acgttaccaa cacggttgat aacccagttc aaattgctgc tgatgctgct   480
398 gatgctgcgc ttcgtggttt cccagaacaa gaaactacta ctgccgttgc ccgttatgca   540
400 ccatttaatg ctatttcaat cttaattggt gctcaaacag tcgtcctgg tgtattaaca    600
402 caatgttctg ttgaagaagc aaccgaattg caattaggaa tgcgtggctt taccgcttat   660
404 gctgaaacta tttcagttta tggtactgac cgggtattta ctgatggtga tgatacacca   720
406 tggtctaaag gattccttgc atcatgttat gcatcgcgtg gtttgaagat gcggtttact   780
408 tcaggtgctg gttcagaagt tttgatgggt tacccagaag gtaagtcaat gttatatctt   840
410 gaagcacgtt gtattttact taccaaggct tcaggtgttc aaggacttca aaacggtgcc   900
412 gtaagttgta ttgaaattcc aggtgctgtt cctaacggta tccgtgaagt tcttggtgaa   960
414 aacctattat gtatgatgtg tgatattgaa tgtgcttctg gttgtgacca agcatactca  1020
416 cactcagata tgcggcgtac tgaacggttt attggtcaat ttattgccgg tactgattac  1080
418 attaattctg gttactcatc aactcctaac tacgataaca cctttgctgg ttcaaacacc  1140
420 gatgcaatgg actacgatga catgtatgtt atggaacgtg acttaggtca atactatggt  1200
422 attcacccag ttcaagaaga aacaattatt aaggctcgta caaggctgc taaggcatta   1260
424 caagctgtat ttgaagatct tggactacct aagattactg atgaagaagt tgaagctgct  1320
426 acatatgcta cactcatga tgacatgcca aaacgtgaca tggttgcaga tatgaaagcc   1380
428 gctcaagata tgatggatcg tggcattact gctattgata ttattaaggc tctttataac  1440
430 catggattta aggatgttgc tgaagctgta ttgaaccttc aaaagcaaaa ggttgtcggt  1500
432 gattccttc aaacttcatc aatctttgac aaggattgga atatcacttc tgccgtaaat   1560
434 gacgggaatg actaccaagg tccaggtact ggataccgtc tatatgaaga caaggaagaa  1620
436 tgggatcgaa tcaaagatct tccattcgca cttgatccag aacacttgga actatag      1677
439 <210> SEQ ID NO: 5
440 <211> LENGTH: 236
441 <212> TYPE: PRT
442 <213> ORGANISM: Lactobacillus reuteri
444 <400> SEQUENCE: 5
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450 Leu Ser Glu Thr Asn Gln Ile Asp Thr Lys Ile Asp Phe Asp Lys Ser
451                 20                  25                  30
454 Asn Asp Ser Thr Ala Thr Ala Thr Gln Glu Val Gln Gln Pro Asn Ser
455             35                  40                  45
458 Lys Ala Val Pro Glu Lys Lys Leu Asp Trp Phe Gln Pro Val Gly Glu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/26/2006
PATENT APPLICATION: US/10/594,417   TIME: 11:46:13

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\10262006\J594417.raw**

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:27,28,29,30,31,32,33,34,35,36,37,38,39,40,46,47,48,49,50,51,52,71,72,73
Seq#:74,75

VERIFICATION SUMMARY   DATE: 10/26/2006
PATENT APPLICATION: **US/10/594,417**   TIME: 11:46:13

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\10262006\J594417.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Raw Sequence Listing before editing
(for reference only)

IFWO

RAW SEQUENCE LISTING   DATE: 10/23/2006
PATENT APPLICATION: US/10/594,417   TIME: 17:25:17

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\10232006\J594417.raw

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     5 <120> TITLE OF INVENTION: Method for producing 1,3-propanediol and 3-hydroxypropionic
acid
     7 <130> FILE REFERENCE: PH-2376-PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/594,417
C--> 9 <141> CURRENT FILING DATE: 2006-09-26
     9 <150> PRIOR APPLICATION NUMBER: JP 2004-093417
    10 <151> PRIOR FILING DATE: 2004-03-26
    12 <150> PRIOR APPLICATION NUMBER: JP 2004-124524
    13 <151> PRIOR FILING DATE: 2004-04-20
    15 <160> NUMBER OF SEQ ID NOS: 75
    17 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

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  3691 <211> LENGTH: 50
  3692 <212> TYPE: DNA
  3693 <213> ORGANISM: Artificial
  3695 <220> FEATURE:
  3696 <223> OTHER INFORMATION: synthetic DNA
  3698 <400> SEQUENCE: 75
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E--> 3708 1/60

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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/23/2006
PATENT APPLICATION: US/10/594,417   TIME: 17:25:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\10232006\J594417.raw**

<u>**Invalid <213> Response:**</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:27,28,29,30,31,32,33,34,35,36,37,38,39,40,46,47,48,49,50,51,52,71,72,73
Seq#:74,75

VERIFICATION SUMMARY   DATE: 10/23/2006
PATENT APPLICATION: **US/10/594,417**   TIME: 17:25:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\10232006\J594417.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3708 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:51 SEQ:75
L:3708 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:3708 M:252 E: No. of Seq. differs, <211> LENGTH:Input:50 Found:51 SEQ:75